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Application of molecular techniques in population genetic studies of cystic fibrosis in the Netherlands

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General introduction

1.1 Delineation of and research into cystic fibrosis

Cystic fibrosis (CF) is the most common lethal autosomal recessive disorder affecting Caucasian populations, with a generally quoted birth prevalence of one in 2500 [1].

Table 1. Historical perspectives of cystic fibrosis research.

1936	Report of a child with the clinical features of cystic fibrosis.	[2]
1938	First detailed description of the clinical features and pathology of CF: "Cystic fibrosis" of the pancreas.	[3]
1945	Recognition of the role of sticky mucus as a cause of many of the symptoms: "Mucoviscidosis".	[4]
1946	Suggestion of an autosomal recessive inheritance pattern for CF.	[5]
1953	Investigation of acute salt loss caused by excessive sweating in babies with CF, during a heat-wave.	[6]
1959	Development of the pilocarpine iontophoresis method for sweat testing.	[7]
1981	Description of altered electrical properties of CF respiratory epithelium associated with abnormalities of both sodium and chloride transport.	[8]
1983	Documentation of chloride impermeability of CF sweat gland ducts.	[9]
1985	Mapping of the CF gene to a small segment of the long arm of chromosome 7q, using restriction fragment length polymorphisms (RFLP).	[10]
1987	Linkage disequilibrium between the markers XV2C/KM19 and cystic fibrosis was observed.	[11]
1989	Cloning of the CF gene and description of a cDNA sequence.	[12]
1989	Identification of the $\Delta F508$ mutation in approximately 70 percent of the mutations.	[13]
1991	Report of the total genomic sequence of the CFTR gene.	[14]
1994	Description of more than 500 different CF mutations.	[15]

The disease is characterized by abnormal secretions of the exocrine glands which cause chronic obstruction and infection of the respiratory tract, meconium ileus, pancreatic insufficiency, and elevated levels of sweat electrolytes. Rochholz (Almanac of Children's Songs and Games from Switzerland, 1857) described "The child will soon die whose brows tastes salty when kissed". Table 1 shows important data on the delineation of and research into CF during the past 60 years.

1.2 The CFTR gene and its mutations

The gene responsible for cystic fibrosis (CF) has been identified in 1989 [12,13,16]. It is located on the long arm of chromosome 7, region 7q31.2 [17]. The gene is approximately 230,000 kb in size and contains 27 exons [14]. The encoded mRNA is about 6.5 Kb long. The gene codes for the 1480 amino acid cystic fibrosis transmembrane conductance regulator (CFTR) protein, with a molecular mass of 168,138 dalton. CFTR is a cAMP-induced chloride channel [18-30], which is located in epithelial tissues, including pancreatic ductal cells, salivary glands, intestine, lung, testis and endometrium [31-34]. Defective regulation of the chloride channel, caused by different mutations in the CF gene, results in desiccation of secretions, increase in the viscosity of mucus and a decrease in mucociliary clearance. The primary sequence of CFTR suggests that it is a transmembrane protein which consists of five domains (Figure 1): two membrane-spanning domains, each composed of six putative transmembrane segments; two nucleotide-binding domains; and a unique regulatory (R) domain [35,36]. The membrane-spanning domains contribute to the formation of the Cl⁻ channel pore. The nucleotide-binding domains and the regulatory domain control the channel activity through an interaction with cytosolic nucleotides. Phosphorylation of the regulator domain by cAMP-dependent kinase is required for the channel to open [37-39]. In addition to this function, the complex expression pattern of the gene and the varied degree of the clinical manifestations in different organs and tissues suggest that CFTR may have other activities [40-45].

Thus far more than 500 presumed mutations have been identified in the CFTR gene in the past 5 years [15]. These mutations can be divided in missense- (42%), frameshift- (23%), nonsense- (16%), splice defect- (16%) and deletion mutations

(4%). The distribution of mutations over the gene is nonrandom, with the highest density in NBF1 (14.4%) and to a lesser extent in NBF2 (10.8%) (Figure 1). Most of the CF mutations have been identified among patients of Caucasian ancestry. The population variation of CF mutations in Europe has been well documented by the Cystic Fibrosis Consortium [46].

Figure 2 shows four different mechanisms by which CF mutations disrupt the CFTR function [36]. **Class 1 mutations:** Mutations (G542X, 621+G->T, etc) that cause defective protein production by premature termination signals as a consequence of affected splice sites, frameshifts or nonsense mutations [35,47,48]. These mutations result in a shortage of CFTR Cl⁻ channels in affected epithelia since little or no full-length protein is produced. **Class 2 mutations:** Several mutant forms of CFTR fail to be transported correctly, which results in defective protein processing. Experiments with other proteins suggest that class 2 mutations (Δ F508, S559T, N1303K, etc) cause an incorrect folding of CFTR. Cellular mechanisms recognise mutant CFTR as abnormal and mark the protein for degradation

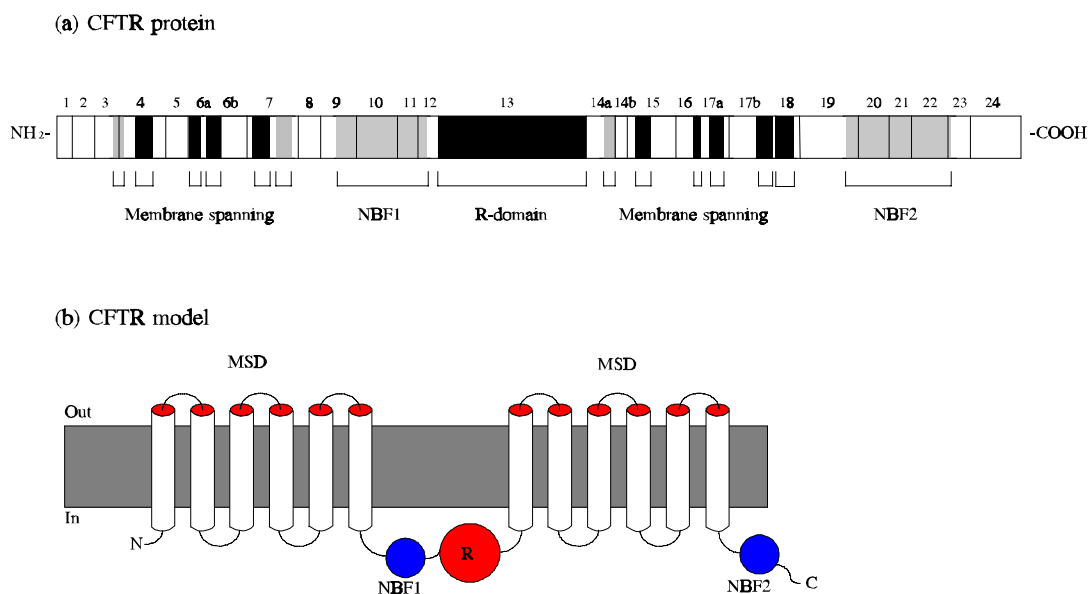


Figure 1. CFTR contains 27 exons and consists of five domains: two membrane-spanning domains (MSD), two nucleotide-binding domains (NBF1 and 2), and a regulatory (R) domain. (Adapted from Tsui and Buchwald)

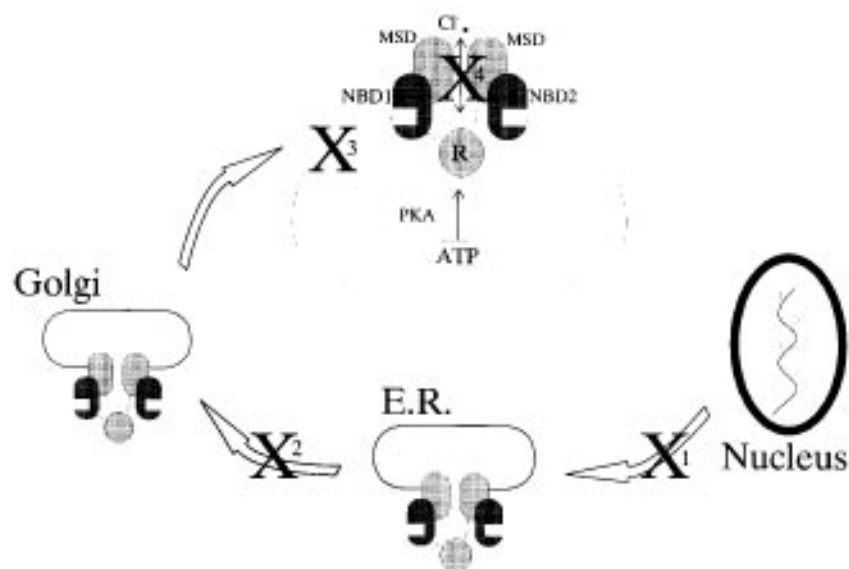


Figure 2. Biosynthesis and function of CFTR in an epithelial cell and action mechanisms of CF mutations. PKA, cAMP-dependent protein kinase; MSD, membrane-spanning domain; NBD, nucleotide-binding domain, R, regulatory domain; X1-4, Class 1-4 mutations; ER, endoplasmatic reticulum. (Adapted from Welsh and Smith)

nucleotide-binding domains (G551D, G551S, A455E, etc). [49,50]. **Class 3 mutations:** Defective regulation by mutations in the NBDs. Intracellular ATP regulates the opening of CFTR Cl⁻ channels through direct interaction with the nucleotide binding domains. Mutations in these domains, therefore, can alter the channel function. **Class 4 mutations:** Mutations (R117H, R334W, etc) that have been identified in the membrane spanning domains, which are thought to contribute to the channel pore [51]. This results in the generation of less Cl⁻ current because the rate of ion flow is reduced.

It is difficult to predict the clinical phenotype from a certain genotype. First, there is a diversity in the clinical phenotype, even within the same genotype. Variability may result from environmental factors and genetic background. Secondly, clinical abnormalities are difficult to predict in compound heterozygotes. Thirdly, patients may bear more than one mutation within the same CFTR gene, of

which only one has been identified. The state of pancreatic function allows discrimination of different phenotypes. Class 1 and 2 mutations are associated with a severe pancreatic-insufficient phenotype, while class 3 and 4 mutations show a normal pancreas function.

Approximately 70% of the CF chromosomes harbour a three basepair deletion in CFTR, which removes the phenylalanine residue at amino acid 508 of the predicted CFTR polypeptide ($\Delta F508$) [46]. The estimates of the age of the $\Delta F508$ mutation vary from 3,000 to 52,000 years [52-55]. According to the latter study, in which microsatellites were used in different CF populations in Europe, the $\Delta F508$ mutation arose at least 52,000 years ago in a population genetically distinct from the present European population. The mutation was introduced in Europe in different periods. The first spread was during the Palaeolithic period. The Basque population is believed to be a Palaeolithic population [56], and has a high relative frequency of $\Delta F508$ (88%) [53]. Later introduction of $\Delta F508$ in Central and Northern Europe (Neolithic period) increased the frequency of this mutation in these regions. The relative $\Delta F508$ frequencies are shown in Figure 3 [46]. The highest frequency per country can be found in Denmark (0.88), while the frequency decreases in Southern and Eastern directions.

1.3 Possibilities for genetic modification

A. Mouse models

The mouse homolog of the human CFTR gene was cloned in 1991 [57]. The mouse protein is 78% identical to the human CFTR, with a high conservation in the transmembrane and nucleotide-binding domains. A mouse model for cystic fibrosis made by gene targeting was first described in 1992 [58]. The murine CFTR gene in embryonic stem cells was inactivated by targeted insertion of a neomycin gene. This resulted in a frame stop codon in exon 10. Numerous mutant mice have been produced using this strategy [59-63]. Almost all mutant CF/CF mice displayed many features common to young CF patients, including failure to thrive, meconium ileus, alteration of mucous and serous glands. This resulted in death due to intestinal obstruction before 40 days of age.

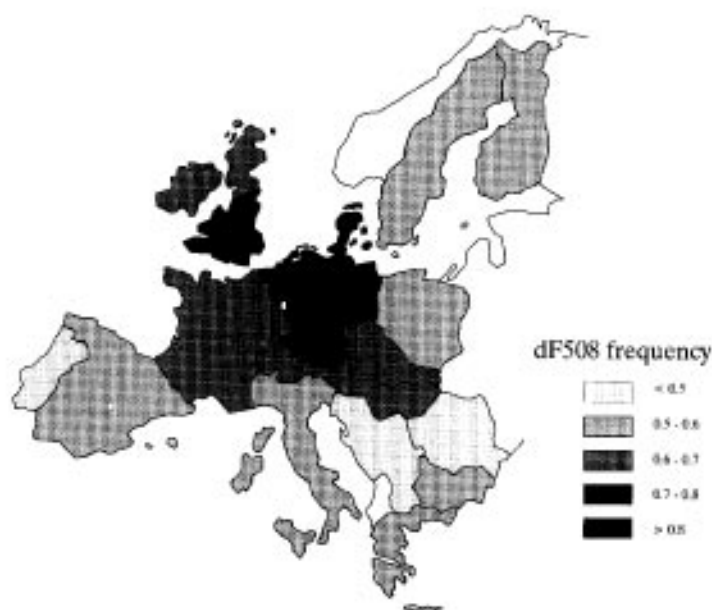


Figure 3. Relative frequency of the $\Delta F508$ mutation in West and Central European populations. The dark shaded areas show a higher $\Delta F508$ frequency compared with the light shaded regions. No data were available from Norway, Luxembourg, Albany and Eastern Europe. The high relative frequency of $\Delta F508$ in the Basque population was averaged with the mutation frequency found in the rest of Spain.

One mutant mouse showed mild focal pulmonary atelectasis, consistent with presymptomatic lung disease, and mild dilatation of salivary ducts [60]. No evidence was obtained for abnormal pancreatic histology or defective reproductivity. The absence of pulmonary disorders in mice can be explained by the late onset of manifestations in humans. By alleviating the intestinal obstruction in CF mice, there is a possibility to observe more of the symptoms of human CF. However some of the differences between the human and mouse phenotypes may be related to tissue-specific patterns of expression of CFTR.

The availability of mouse models provides opportunities for the testing of new therapies and to study the intestinal pathophysiology of CF in greater detail. For example, to determine whether heterozygotes are more protected against exposure to cholera toxin (see 1.5).

B. Somatic gene therapy for cystic fibrosis

The clinical expressions of CF are very broad, although the manifestations in the airways account for more than 95% of the morbidity in CF patients [1]. It is therefore that gene transfer strategies are focused on delivery to the airways. A variety of gene transfer techniques have been used effectively in vitro and in animals: adenoviral vectors, liposome-mediated gene transfer, DNA-ligand complexes and adeno-associated viral (AAV) vectors [64]. The first two therapies are being used in phase I clinical trials involving CF patients.

Several studies indicate that even a low expression (10%) of the CF gene in airway epithelium may provide clinical benefit [65,66]. Healthy CF carriers will have half-normal levels of expression. There are some compound heterozygotes which show mild or normal phenotypes, while they have very low levels of expression [47,67]. This means that there is no necessity to correct all cells and even low levels of expression per cell may be beneficial.

The major goals for somatic gene therapy for cystic fibrosis are (1) to show that the expression of the CF gene in airways epithelium will alleviate lung disease in CF patients and (2) to achieve a lasting expression of the transferred gene.

Table 3. Major advantages and disadvantages of gene transfer systems.

	<u>Advantages</u>	<u>Disadvantages</u>
Adenoviral vectors	1. Highly efficient gene transfer 2. Transfection of many cell types	1. Transient nature of the expression 2. Pathogenicity of the wild type virus 3. No evidence for safe and effective readministration.
DNA-liposome complexes	1. Standardized production of large amounts of vector 2. No risks of viruses 3. Readministrations with minimal host response	1. No persistent expression 2. Low gene expression
DNA ligand complexes	1. See DNA-liposome complexes	1. See DNA-liposome complexes 2. Large size of complexes may complicate escape from the vascular space 3. Peptides can induce immune responses
AAV vectors	1. Stable virus preparations 2. Lack of pathogenicity 3. High-efficiency integration at present	1. Possibility for immune responses 2. No adequate system to produce virus 3. Limitation of insert size to 4.8 kb

This can be performed through a single delivery with persistent expression or by use of a save and effective repetitive delivery system. The biological aspects of various gene transfer systems have been reviewed elsewhere [68,69]. The advantages and disadvantages of these strategies are summarized in table 3.

1.4 Cystic fibrosis prevalence at birth

Cystic fibrosis is the most common autosomal recessive disease in caucasian populations. Birth prevalences have been determined by surveys and range from 1 in 1700 to 1 in 40,000 in various European countries (Table 2). Thus far, estimates based on molecular screening for heterozygotes have not been described in European populations.

The estimates of the birth prevalences show a variability which as a whole or in part may be due to under- or overdiagnosis and under- or overreporting. Alternatively this variability may be due to mechanisms such as foundereffect and genetic drift.

Table 2. Birth prevalences of cystic fibrosis determined in European populations

Czechoslovakia	1 in 2600	1962 [70]
	1 in 2800	1964 [71]
	1 in 2700	1967 [72]
	1 in 3400	1970 [73]
	1 in 3300	1970 [74]
	1 in 5440	1972 [75]
Denmark	1 in 4500	1972 [76]
	1 in 4760	1988 [77]
England	1 in 3000	1967 [78]
	1 in 4100	1967 [79]
	1 in 2000	1968 [80]
	1 in 3000	1972 [81]
	1 in 2500	1988 [82]
Finland	1 in 40000	1972 [83]
France	1 in 3300	1961 [84]
	1 in 1700-2000	1971 [85]
	1 in 2000	1973 [86]
	1 in 1800	1974 [87]
Germany	1 in 3200	1978 [88]
	1 in 3300	1963 [89]
	1 in 3000	1968 [90]
	1 in 2000	1975 [91]

Table 2. (Continued)

Ireland	1 in 1800	1976 [92]
Italy	1 in 1100-3500	1973 [93]
	1 in 2700	1976 [94]
	1 in 2000	1985 [95]
	1 in 3600	1975 [96]
Netherlands	1 in 1700	1959 [Cited by Clarke, 97]
N-Ireland	1 in 1900	1979 [98]
	1 in 900-2500	1970 [99]
Poland	1 in 7700	1962 [100]
Sweden	1 in 4000	1970 [101]
	1 in 3500	1976 [102]
	1 in 2200-4500	1982 [103]
	1 in 2900	1976 [104]
Switzerland	1 in 3000	1973 [105]
Turkey		

1.5 What causes the high frequency of cystic fibrosis ?

The high birth prevalence of cystic fibrosis of about one in 2500 in the Caucasian population [1] has been discussed in many papers. A variety of mechanisms has been suggested to account for this high frequency: genetic drift [106], high mutation rate [107], meiotic drive and increased fertility of CF carriers [108], genetic heterogeneity [109], heterozygote advantage [109-113] and segregation distortion of CF alleles [108,114,115] . Heterozygote advantage is the most likely explanation. A positive selection of approximately 2% [113] would be sufficient to maintain the CF gene frequency at current levels.

The best understood example of heterozygote advantage remains sickle cell haemoglobin, and the protection it confers against malaria. In case of CF, abnormally functioning chloride channels could lead to increased protection against bacterial toxin-mediated diarrhoea. Some of the diseases which have been suggested as the balancing agent for CF are: influenza [116,117], syphilis [118], malaria [119], bubonic plague [112] and cholera [119-122]. Gabriel et al. [123] showed reduced diarrhoea in the cystic fibrosis heterozygote mouse compared with the normal mouse after exposure to cholera toxin. This effect, however, has not been studied in human populations so far.

1.6 Screening for cystic fibrosis carriers

The investigation of the validation of a mouthwash procedure and of the determination of the carrier prevalence in the Netherlands (Chapters 2 and 3) can partially be considered as preparatory studies for possible population-based screening programmes. Immediately upon the cloning of the CF gene in 1989, intensive discussions began regarding the feasibility and appropriateness of offering carrier testing to the general population. Wilfond and Fost [124] have reviewed many of the concerns in detail. The following arguments against population screening have been raised. (1) It is too expensive and not cost-effective. (2) It is not possible to identify all at-risk couples. (3) Families do not wish to avoid the disease. (4) Prevention through abortion is morally objectionable. (5) A cure for the disease is possible. (6) The personnel needed for genetic counselling are not available. (7) Many couples are left at slightly increased risk. (8) There is a risk of discrimination regarding insurance or employment. The following arguments in favour of carrier testing have been raised. (1) Testing will become less expensive and be cost-effective. (2) The majority of couples at-risk can be identified. (3) Many couples wish to avoid the disease through various reproductive options. (4) There is an obligation to inform the public about the availability of carrier testing. Pilot studies for CF testing can address some of these issues.

Investigations in different groups of people revealed a positive attitude toward carrier screening [125-128]. The American Society of Human Genetics and the National Institutes of Health stated that carrier screening would be desirable only if 90-95% of mutations can be detected. Present data suggest that the sensitivity can be well above 90% in some Northern European populations, for instance 98% in Belgium [129], 98% in a Celtic population in Brittany [130] and 99% in Wales [131]. The $\Delta F508$ mutation can be detected by simple gel electrophoresis in material like blood samples, dried blood spots, mouthwashes, mouthbrushes or fetal cells. The application and validation of the mouthwash procedure for the DNA isolation out of buccal cells is described in Chapter 2. Most laboratories now test routinely for from 10 to over 30 common CF mutations using forward or reverse ASO methods [132] and the Amplification Refractory Mutation System [133]. Solid-phase methods based on ligation detection, single base sequencing and other tests offer great promise for the development of highly

automated procedures for the economical analysis of dozens of mutations simultaneously [134]. An economic two-step laboratory approach can be used for mutation detection [135]. In the first step only a few mutations will be determined and only the partners of identified carriers will be tested for additional mutations. The development of economic highly automated procedures for mutation analysis and the positive attitude toward carrier testing will strongly increase the demand for population based screening.

1.7 Identity By Descend (IBD) analysis

Haplotype sharing analysis is based on linkage disequilibrium of polymorphic loci with a disease gene. In previous investigations extensive linkage studies have been applied for the mapping of rare disease alleles. Although these studies provided valuable contributions toward the mapping of mutated genes, a few disadvantages can be observed using the traditional gene localization methods. (1) It is difficult to obtain adequate family material and large pedigrees. (2) After the selection of families all members should be examined concerning clinical features. (3) Hundreds of markers should be involved in a complete genome search. (4) Costs of material and manpower are high.

Identity by descent (IBD) analysis is an alternative association study method, in which unrelated patients in a founder population can be selected for gene mapping. Patients with identical genetic diseases are likely to share the disease gene and an area around that gene from a common ancestor. The size of the expected shared area depends on the number of meioses connecting the different persons, because in time the size of the region will be reduced by crossovers. The larger the shared area the closer the connection with a common predecessor from whom the gene originates [136]. The size of the shared regions allows IBD to be used in the genetic mapping of genes. Gruis et al. [137] described haplotype sharing in presumedly unrelated patients from a founder population. This sharing was determined by identity by descent of an area surrounding the disease gene. Houwen et al. [138] showed that mapping within 2 cM was possible using only three affected persons.

There are some points of importance which must be taken into consideration

when using IBD mapping. (1) The patients samples have to be collected in an established founder population. (2) For the assignment of haplotypes it is necessary to analyze also DNA of the parents. In case the phase is unknown it is possible to assign haplotypes according to their frequency. This, however, will reduce the power of the test drastically. (3) The allele frequency of the various markers used with IBD mapping has to be established in a control group within the same founder population.

A two step IBD approach can be used for gene mapping. In the first step a few not too far related patients with an identical genetic disorder can be haplotyped for a rough mapping of the disease gene. Markers can be selected with intervals of about 20 cM. This means that 100-200 markers will cover the whole genome. Fine mapping can be performed on the shared regions in a group of seemingly unrelated patients within a restricted area. These regions will be haplotyped then with highly polymorphic markers with relative distances of about 2 cM. This method allows fast and relative cheap gene mapping. A pooling strategy has been described [139] in which DNA from affected individuals were pooled and used as a PCR template for microsatellite primers. The amplification product of pooled DNA samples reflects all alleles represented in the pooled population. The relative frequency of the alleles correlates with the intensity of each allelic band in the gel after electrophoresis. In case of linkage disequilibrium of the microsatellite with a disease genotype there will be a shift in allele frequencies towards a homozygous allele pattern in the affected DNA pool. The use of the pooling strategy facilitates the identification of the disease loci by reducing the number of amplification products and gel lanes. Differences between control and affected pools can easily be examined, without the need of assigning individual genotypes.

IBD analysis can also be used for determination of the origins of certain mutations or the relationships of patients with identical genetic diseases. In case of cystic fibrosis, mutations have been reported which occur predominantly in certain countries [46]. The mutations may have originated in these countries not very long ago. An example is the A455E CF mutation, which is mainly detected in Southern-Holland and in Canada among certain French Canadians. It is likely that patients with this mutation have a common not too far predecessor. Chapter 6 describes the IBD analysis in Dutch and French Canadian patients.

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